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32. The method of claim 29, wherein said simple or cryptically simple sequence has a repeat length of 3 to 6 nucleotides, each of said primers has a length of 15 to 25 nucleotides and 2 to 50 primer pairs are used.

33. The method of claim 30, wherein said simple or cryptically simple sequence has a repeat length of 3 nucleotides.

34. The method of claim 32, wherein said simple or cryptically simple sequence has a repeat length of 3 nucleotides.

35. A kit for performing analysis of polymorphism in simple or cryptically simple sequences, comprising:

- a) at least one vessel containing a mixture of primers constituting 1 to 50 primer parts; wherein each of said primer pairs is composed of a first primer complementary to a nucleotide sequence flanking said simple or cryptically simple DNA sequence on the 5' side of said simple or cryptically simple DNA sequence and a second primer complementary to a nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 3' side of said simple or cryptically simple DNA sequence; wherein said first and second primers each anneal to a single site in said DNA template and wherein the annealing sites are separated by 50 to 500 nucleotides of template DNA;

- b) a vessel containing a template DNA that has a nucleotide sequence including a simple or cryptically simple sequence for assaying positive performance of the method.

36. The kit of claim 35, wherein at least one primer of each primer pair is labeled with a fluorescent or a radioactive label.

37. The kit of claim 35, wherein said simple or cryptically simple sequence has a repeat length of 3 to 6 nucleotides and each of said primers has a length of 15 to 25 nucleotides.

38. The kit of claim 35, wherein said simple or cryptically simple DNA sequence is located adjacent to or within a genetically defined locus such that said simple or cryptically simple DNA sequence can serve as a marker for said locus.

39. The kit of claim 38, wherein at least one primer of each primer pair is labeled with a fluorescent or a radioactive label.

40. A method for determining length polymorphisms in a simple or cryptically simple sequence in one or more DNA regions of one or more subjects, which comprises:

- a) providing at least one DNA sample, comprising a template DNA consisting essentially of a nucleotide sequence that includes i) a simple or cryptically simple sequence having a trinucleotide repeat motif and ii) nucleotide sequences flanking the simple or cryptically simple sequence, from at least one subject;
- b) annealing at least one primer pair to the template DNA of each of said DNA samples, wherein said primer pair is composed of a first primer complementary to the nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 5' side of said simple or cryptically simple DNA sequence and a second primer complementary to the nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 3' side of said simple or cryptically simple DNA sequence; wherein said first and second primers each anneal to a single site in said template DNA and the

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sequence of the template DNA between the sites where said primers anneal is 50 to 500 nucleotides in length;

- c) performing at least one primer-directed polymerase chain reaction upon said template DNA having said primers annealed thereto, so as to form at least one polymerase chain reaction product;
- d) separating the products of each polymerase chain reaction according to their lengths;
- e) analyzing the lengths of the separated products to determine the length polymorphisms of the simple or cryptically simple sequences.

41. A method for analyzing polymorphism in at least one locus in an DNA sample comprising a DNA template, said method comprising:

- a) annealing said DNA template with at least one pair of primers, wherein said primer pair is composed of a first primer complementary to a nucleotide sequence flanking said simple or cryptically simple DNA sequence on the 5' side of said simple or cryptically simple DNA sequence and a second primer complementary to a nucleotide sequence flanking the simple or cryptically simple DNA sequence on the 3' side of said simple or cryptically simple DNA sequence; wherein said first and second primers each anneal to a single site in said DNA template and wherein the annealing sites are separated by 50 to 500 nucleotides of template DNA;
- b) performing at least one primer-directed polymerase chain reaction upon said template DNA having said primers annealed thereto, so as to form at least one polymerase chain reaction product;
- c) separating the products of each polymerase chain reaction product according to their lengths; and
- d) analyzing the lengths of the separated products to determine the length polymorphisms of said simple or cryptically simple sequences,

wherein said DNA template includes at least one sequence consisting essentially of a simple or cryptically simple DNA sequence having a repeat motif length of 3 to 10 nucleotides and nucleotide sequences flanking said simple or cryptically simple DNA sequence effective for annealing said at least one pair of primers.

42. A kit for analyzing polymorphism in at least one locus in an DNA sample, comprising:

- a) at least one vessel containing a mixture of primers constituting between 1 and 50 of said primer pairs;
- b) a vessel containing a polymerizing enzyme suitable for performing a primer-directed polymerase chain reaction;
- c) a vessel containing the deoxynucleotide triphosphates adenosine, guanine, cytosine and thymidine;
- d) a vessel containing a buffer solution for performing a polymerase chain reaction;
- e) a vessel containing a template DNA comprising i) a simple or cryptically simple nucleotide sequence having a repeat motif length of 3 to 10 nucleotides and ii) nucleotide sequences flanking said simple or cryptically simple nucleotide sequence that are effective for annealing at least one pair of said primers, for assaying positive performance of the method.

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